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## **Characterization of a transport activity for long-chain peptides in barley mesophyll vacuoles**

Ramos, M S ; Abele, R ; Nagy, R ; Grotemeyer, M S ; Tampé, R ; Rentsch, D ; Martinoia, E

**Abstract:** The plant vacuole is the largest compartment in a fully expanded plant cell. While only very limited metabolic activity can be observed within the vacuole, the majority of the hydrolytic activities, including proteolytic activities reside in this organelle. Since it is assumed that protein degradation by the proteasome results in the production of peptides with a size of 3-30 amino acids, we were interested to show whether the tonoplast exhibits a transport activity, which could deliver these peptides into the vacuole for final degradation. It is shown here that isolated barley mesophyll vacuoles take up peptides of 9-27 amino acids in a strictly ATP-dependent manner. Uptake is inhibited by vanadate, but not by NH<sub>4</sub><sup>+</sup>, while GTP could partially substitute for ATP. The apparent affinity for the 9 amino acid peptide was 15  $\mu$ M, suggesting that peptides are efficiently transferred to the vacuole in vivo. Inhibition experiments showed that peptides with a chain length below 10 amino acids did not compete as efficiently as longer peptides for the uptake of the 9 amino acid peptide. Our results suggest that vacuoles contain at least one peptide transporter that belongs to the ABC-type transporters, which efficiently exports long-chain peptides from the cytosol into the vacuole for final degradation.

DOI: <https://doi.org/10.1093/jxb/erq397>

Posted at the Zurich Open Repository and Archive, University of Zurich

ZORA URL: <https://doi.org/10.5167/uzh-53835>

Journal Article

Accepted Version

Originally published at:

Ramos, M S; Abele, R; Nagy, R; Grotemeyer, M S; Tampé, R; Rentsch, D; Martinoia, E (2011). Characterization of a transport activity for long-chain peptides in barley mesophyll vacuoles. *Journal of Experimental Botany*, 62(7):2403-2410.

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**Characterization of a transport activity for long-chain  
peptides in barley mesophyll vacuoles**

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29 Key words: ABC transporter, Peptide transport, Transport, Vacuole

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31 Running title: Transport of long-chain peptides into barley mesophyll

32 vacuoles

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## Abstract

The plant vacuole is the largest compartment in a fully expanded plant cell. While only very limited metabolic activity can be observed within the vacuole, the majority of the hydrolytic activities, including proteolytic activities reside in this organelle. Since it is assumed that protein degradation by the proteasome results in the production of peptide with a size of 3 to 30 amino acids, we were interested whether the tonoplast exhibits a transport activity, which could deliver these peptides into the vacuole for final degradation. Here we show that isolated barley mesophyll vacuoles take up peptides with a size of 9 to 27 amino acids in a strictly ATP-dependent manner. Uptake is inhibited by vanadate but not by  $\text{NH}_4^+$ , while GTP could partially substitute for ATP. The apparent affinity for the 9-mer peptide was 15  $\mu\text{M}$ , suggesting that peptides are efficiently transferred to the vacuole *in vivo*. Inhibition experiments showed that peptides with a chain length below 10 amino acids did not compete as efficiently as longer peptides for the uptake of a 9 amino acid long peptide. Our results suggest that vacuoles contain at least one peptide transporter that belongs to the ABC-type transporters, which efficiently exports long chain peptides from the cytosol into the vacuole for final degradation.

71

## 72 **Introduction**

73

74 Plant vacuoles are multifunctional organelles that play a central role during  
75 the whole plant life. While young cells often contain many small vacuoles,  
76 most of the mature cells have one central vacuole, which occupies up to  
77 90% of the cell volume. Additionally, small vacuoles may be present in such  
78 cells. A large number of substances such as inorganic ions, soluble  
79 carbohydrates, organic acids, amino acids, secondary compounds or  
80 modified xenobiotics, but also hydrolytic and biosynthetic enzymes, can be  
81 found within vacuolar compartments. The vacuole is responsible for  
82 numerous processes, sometimes unique to the plant cell [Martinoia *et al.*,  
83 2007, Hörtensteiner & Feller, 2002]. The negative water potential drives the  
84 uptake of water into the large central vacuole, generating the turgor pressure  
85 that enables the cells to expand, as well as to sustain the shape of non-  
86 lignified plants. The vacuole can serve as a transient storage compartment  
87 for nutrients, which can be released when required for growth and  
88 development. Furthermore, in specialized storage tissues or seeds, storage  
89 vacuole can act as storage compartment for protein. The vacuole plays also  
90 a crucial role in the tight control of cytosolic concentrations of metabolites  
91 and ions for cell homeostasis. Additionally, the vacuole is implicated in  
92 detoxification processes and defence responses by accumulating and  
93 sequestering toxic compounds and defence molecules.

94

95 In order to support the intensive exchanges that occur between the cytosol  
96 and the vacuole a large number of proteins are embedded in the vacuolar  
97 membrane. Two proton pumps, namely the H<sup>+</sup>-ATPase (V-ATPase) and the  
98 H<sup>+</sup>-pyrophosphatase (V-PPase), located in all vacuolar membranes generate  
99 the electrochemical gradient, required to energize a large majority of the  
100 transport mediated by tonoplast proteins [Sze *et al.*, 1999, Maeshima, 2001].  
101 Two other classes of transporters located in the vacuolar membrane mediate  
102 a directly ATP energized transport and allow the accumulation of their  
103 substrates independently from the proton motive force: cation pumps  
104 belonging to the class of the P-type ATPases and ATP-binding cassette  
105 (ABC) transporters [White & Broadley, 2003, Rea, 2007, Yazaki et al. 2009].

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108 The ATP-binding cassette (ABC) transporters constitute a large, diverse,  
109 ubiquitous superfamily, widespread in bacteria, fungi, animal and plant  
110 kingdoms. Most of the ABC proteins are involved in the directly energized  
111 transport of a large variety of substances across various biological  
112 membranes. Compared to all other organisms, plants contain by far more  
113 ABC transporters. Most of them can be grouped in the eight major  
114 subfamilies (A-H), universally shared by living organisms [Verrier *et al.*,  
115 2008]. In plants, ABC proteins have been shown to be implicated in diverse  
116 essential processes such as vacuolar sequestration of xenobiotics, heavy

metal tolerance, pigment accumulation, auxin transport, alkaloid import at the plasma membrane, wax deposition on the cuticle, lipid catabolism, stomatal regulation, disease/pathogen resistance or assembly of redox-active cytosolic Fe/S proteins [Martinoia *et al.*, 1993, Lu *et al.*, 1998, Gaedeke *et al.*, 2001, Shitan *et al.*, 2003, Pighin *et al.*, 2004, Xu & Møller, 2004, Lee *et al.*, 2005, Geisler & Murphy, 2006, Kim *et al.*, 2007, Rea 2007, Yazaki *et al.* 2009]. However, the number of uncharacterized ABC transporters remains high and their implication in plant metabolism still awaits to be discovered.

Peptides are implicated in many different processes occurring in living cells. In mammals they are used for example for antigene processing or as hormones (Parcej and Tampe, 2010,). Furthermore, some antibiotics and anticancer drugs are peptides [Dantzig *et al.*, 1992, Hori *et al.*, 1993]. In bacteria, peptides can be involved in quorum sensing [Swift *et al.*, 1996]. In plants, during the seed germination, peptides are first produced to supply the seedling with reduced nitrogen [Higgins & Payne, 1981, Stacey *et al.*, 2002b]. Three gene families potentially code for peptide transporters. Members of the peptide transporter/nitrate transporter 1 (PTR/NRT1) family recognize di- and tripeptides, while some members of the oligopeptide transport (OPT) family transport predominantly tetra- and pentapeptides, though longer or shorter peptides are sometimes also translocated [Tsay *et al.*, 2007, Rentsch *et al.*, 1995, 2007, Koh *et al.*, 2002, Stacey *et al.*, 2002a,

Waterworth and Bray, 2006, Pike *et al.*, 2009]. In mammals, three members of the ABC transporter superfamily, the so-called TAPs, have been shown to be involved in the transport of longer chain peptides. They reside either in the ER, Golgi or in lysosomal membrane and mediate the transport of peptides ranging from 6 to 59 amino acids [Kelly *et al.*, 1992, Lankat-Buttgereit and Tampé, 2003, Wolters *et al.*, 2005].

Early work on plant vacuoles has shown that vacuoles contain highly active proteases [Boller and Kende, 1979]. It was suggested that these proteases are implicated in cellular protein turnover. However, this hypothesis still awaits confirmation. Proteomic studies using *Arabidopsis* and barley vacuolar membranes have revealed a large number of putative vacuolar transporters with still unknown function, among also TAP homologs (Carter *et al.* 2004, Endler *et al.*, 2006, Jaquinot *et al.*, 2007). We were therefore interested to investigate whether vacuoles exhibit peptide transport activity for larger peptides of a size between 9 and 30 amino acids.

## Material and Methods

*Plant material.* Barley (*Hordeum vulgare* L. cv. Baraka) was grown in a controlled environment chamber (16 h light ( $300 \mu\text{E m}^{-2} \cdot \text{s}^{-1}$ ) / 8 h dark cycle; 22 °C, 60% relative humidity).



*Isolation of intact vacuoles.* Barely mesophyll vacuoles were isolated by a slight modification described in *Rentsch and Martinoia* (1991). After resuspension of the protoplasts, they were collected by centrifugation (10 min, 200 x g) on a cushion of osmotically stabilized Percoll (500 mM sorbitol; 1 mM CaCl<sub>2</sub> (Fluka Buchs, Switzerland); 20 mM MES, pH 6). Protoplasts were suspended in 5 ml of a solution containing 500 mM sorbitol; 30% (v/v) Percoll; 1 mM CaCl<sub>2</sub>; and 20 mM MES, pH 6. This suspension was overlayed with 10 ml medium A (430 mM sorbitol, 25% (v/v) Percoll, 30 mM K-gluconate (Fluka Buchs, Switzerland) and 20 mM HEPES-KOH pH 7.2) and 5 ml medium B (430 mM sorbitol, 30 mM K-gluconate and 20 mM HEPES-KOH pH 7.2). After centrifugation for 10 min at 200 x g, protoplasts were recovered from the upper interface, mixed with 15% (v/v) medium B; and 10 mM EDTA and forced through a syringe without needle to liberate the vacuoles. The protoplasts lysate was suspended in a solution containing 500 mM sorbitol; 20% (v/v) Percoll; and 20 mM HEPES-KOH pH 7.2. The suspension was overlayed with 5 ml of medium B; 0.1% (w/v) BSA (Fluka Buchs, Switzerland); and 0.2 mM DTT and 1 ml medium C (400 mM glycine-betaine, 30 mM K-gluconate and 20 mM HEPES-KOH pH 7.2); 0.1% (w/v) BSA; and 0.2 mM DTT. After centrifugation for 3 min at 300 rpm and 5 min 1200 rpm, vacuoles were recovered from the upper interface. Last purification gradient was repeated with the recovered vacuoles but centrifuged for 5 min at 1500 rpm. The purified vacuoles recovered from the upper interface were completed with Percoll (final concentration 10% (v/v)

Percoll; 500 mM sorbitol; and 20 mM HEPES-KOH pH 7.2) and the suspension was directly used for uptake experiments.

*Uptake experiments.* Uptake of fluorescein-labeled peptides 9-mer: RRYC( $\phi$ )KSTEL, 18-mer: RRYQKSTELRRYC( $\phi$ )KSTEL, and 27-mer: RRYQKSTELRRYQKSTELRRYC( $\phi$ )KSTEL was measured by a slight modification of method described by *Martinoia* et al. (1993). For each condition and time point, five polyethylene microcentrifugation tubes (400  $\mu$ l capacity) were prepared as follows: 70  $\mu$ l of basal medium (22% Percoll pH 7.2, 430 mM sorbitol, 30 mM K-gluconate, 20 mM HEPES-KOH pH 7.2, 0.1% BSA, 0.2 mM DTT) containing 1 mCi  $^3\text{H}_2\text{O}$ , 2  $\mu$ M of one of the fluorescein-labeled peptides and solutes as indicated in the figures were placed in the bottom of the tubes. Experiments were started by the addition of 30  $\mu$ l of the vacuole suspension. Samples were rapidly overlayed with 200  $\mu$ l silicone oil AR 200 and 60  $\mu$ l medium C described in the paragraph above. Incubation was interrupted by centrifugation at 10,000  $\times g$  for 20 s. The fluorescent peptides contained in the medium C were quantified using a fluorescence plate reader ( $\lambda$  ex/em 485/520 nm; Fusion, Packard).  $^3\text{H}_2\text{O}$  equilibrates rapidly between the medium and the vacuolar space and was used to quantify the number of vacuoles by scintillation counting.

For competition, randomized peptide libraries were added (Uebel et al 1997)

## Results

### Time-dependent uptake of fluorescein-labeled peptides

In order to characterize a hypothetical vacuolar peptide transporter in plants, we isolated highly purified barley mesophyll vacuoles. Transport assays were performed using three peptides of different sizes, a 9 amino acid (aa) (RRYC( $\phi$ )KSTEL), a 18 aa (RRYQKSTELRRYC( $\phi$ )KSTEL) and a 27 aa (RRYQKSTELRRYQKSTELRRYC( $\phi$ )KSTEL) peptide, where  $\phi$  symbolizes the fluorescein fluorophore. Uptake experiments were performed at a peptide concentration of 2  $\mu$ M in the presence or absence of 4 mM MgATP. Uptake of all three peptides was strictly MgATP-dependent (Fig. 1A, B and C). In the absence of MgATP, no uptake could be observed, while in the presence of MgATP, efficient peptide uptake occurred which was linear for at least 20 minutes. The ATP-dependent transport rates increased with the size of the peptide. They were  $0.59 \pm 0.14$ ,  $0.88 \pm 0.13$  and  $1.78 \pm 0.50$  pmol ml<sup>-1</sup>·min<sup>-1</sup> for the 9, 18 and 27 amino acid long peptide, respectively.

### Energization of the peptide transporter

Vacuoles have an acidic pH; therefore, the ATP-dependent peptide transport into barley vacuoles might occur by a secondary energized mechanism utilizing the proton motive force or directly by MgATP-hydrolysis by ABC-type transporters. To distinguish between these two mechanisms, we performed transport experiments using different inhibitors. Since uptake was

linear for at least 20 min, peptide uptake rates were determined by subtracting the 2 min from the 20 min value. This allowed correcting for unspecific adsorption. Compared to MgATP, MgGTP, which is known to be able to partially substitute for MgATP in the case of ABC transporters, was able to catalyze the peptide transport to 30 to 50% (Fig. 2). Interestingly, MgGTP was more efficient in energizing the transport of the longer peptides. The non-hydrolysable ATP analogue, AMP-PMP failed to catalyze peptide transport, indicating that energy is required to drive the transport of the peptides. Valinomycin, a  $K^+$  specific ionophore, which dissipates the membrane potential, and bafilomycin, a highly specific inhibitor of the vacuolar  $H^+$ -ATPase, did not inhibit the transport of the different peptides. Interestingly, valinomycin had even a promoting effect in case of the 27-mer. Vanadate, is an efficient inhibitor for most ABC-type protein-mediated transport processes, also inhibited the ATP-driven peptide transport. This inhibition was more pronounced (80%) for the shorter peptides, while transport of the 27 aa peptide was only inhibited by 50% (Fig. 2). Since the inhibitory effect of vanadate at a concentration of 0.5 mM was different for short and long peptides, we wondered whether the concentration-dependence of the vanadate inhibition was different for the nine and twenty-seven amino acid long peptides. Raising the vanadate concentration did not consistently lead to a higher inhibition than observed at 0.5 mM (Fig. 3). Furthermore, the concentration required to inhibit the transport rate to 50% of the maximal vanadate inhibition, were 75  $\mu$ M and 80

μM, for the 9 aa and 27 aa peptide, respectively. Similar IC<sub>50</sub> values have been already reported for other ABC mediated transport processes [Wolters *et al.*, 2005].

We determined also the concentration dependency for MgATP using the 9 aa peptide. The data clearly fitted by the Michaelis-Menten equation with an apparent  $K_m^{MgATP}$  value of  $146.6 \pm 93.7$  μM (Fig. 4), a value which is similar to affinity reported for other ABC transporters [Rea *et al.*, 1998].

### **Concentration-dependency of the peptide transporter and impact of the peptide length**

As shown in Fig. 5, the transport rates for the 9 aa peptide followed a Michaelis-Menten kinetic. As this experiment required a large amount of peptide, increasing the concentration until reaching saturation was not possible. From the data available, an apparent  $K_m^{pep}$  of about 15 μM and a maximal transport activity ( $V_{max}$ ) of about 8 pmol μl<sup>-1</sup>•min<sup>-1</sup> were determined.

Furthermore, we were interested to investigate how the transport of the 9 aa peptide was affected by peptides of different length. To this end, we performed uptake experiments using 2 μM of the fluorescent 9 aa peptide in the presence of 20 μM of unlabeled randomized peptide libraries of increasing size ( $X_i$ ,  $i = 4, 7, 10, 11, 17, 23, 35$  and 53 residues, Fig. 6, see Materials and Methods). The advantage of these randomized peptide libraries is that they do not rely on a single sequence. The transport activity of the labeled peptide showed no reduction in the presence of a small

peptide of 4 amino acid residues. The peptide with 7 aa exhibited a 20% inhibition, while the peptide with 10 and more aa inhibited uptake of the 9 aa peptide by about 50%. This value can be expected taking into account a  $K_m$  of 15 to 20  $\mu M$ . Longer peptides had the tendency to be slightly more inhibitory. However, this inhibition study suggests that while the transport activity increases with the size of the peptide the affinity of the transporter for the longer chain peptides remains the same.

## Discussion

Peptides play an important role not only in nitrogen nutrition but also in various processes occurring within living cells [Higgins and Payne, 1981, Stacey *et al.*, 2002b]. Despite the identification of a large number of putative peptide transporters in the *Arabidopsis* genome, little is known about their activity, localization and involvement in the whole plant metabolism. All plant peptide transporters described so far transport small peptides up to 5 amino acids. Only AtOPT6 was shown to transport also peptide as long as 13 amino acids [Pike *et al.*, 2009]. Large peptides may be generated by endoproteases as well by the proteasome complex. The universal ubiquitin-proteasome complex pathway is the best-defined protein degradation pathway [Smalle & Viestra, 2004]. The proteasome complex exhibits three proteolytic activities, a chymotrypsin-like, a trypsin-like, and a peptidyl-

301 glutamyl peptide-hydrolyzing activity. Combined together, these proteases  
302 generate peptides of a size between 3 and 30 amino acids. The universal  
303 ubiquitin-proteasome complex pathway together with the less-well  
304 characterized cytoplasmic and plastid degradation pathways produce the  
305 major part of the peptides found in the plant cell [Sakamoto, 2006]. So far,  
306 the subsequent step of this protein turnover process, *i.e.* the final  
307 degradation of the resulting peptides leading to the production of amino  
308 acids, which can be reused for *de novo* protein synthesis, is less understood.  
309 Since a long time, the presence of hydrolytic enzymes in vacuoles had been  
310 demonstrated [Boller and Kende, 1979]. It was however not clear, whether  
311 peptides have to be imported into the vacuole for their final degradation.  
312 In contrast to plants, transporters for long chain peptides have been well  
313 characterized in animals. These transporters belong to the so-called TAP  
314 (Transporter associated with Antigenic Processing) family. In humans, TAP1  
315 (ABCB2) and TAP2 (ABCB3) form a heterodimer which transports peptides  
316 generated by the proteasome complex into the ER where they are loaded  
317 onto a newly synthesized MHC class I complex. The MHC I-peptide complex  
318 is exported to the cell surface to be exposed to T-cells. By means of its  
319 function, this heterodimer was shown to play a central role in the immune  
320 system. (Trowsdale *et al.*, 1990, Bahram *et al.*, 1991, Higgins *et al.*, 1992,  
321 Abele and Tampé, 2004). . In mammals the third member of this family is  
322 the so-called TAP-like, which forms homodimers and is a peptide transporter

located in the lysosomal membrane [Wolters *et al.*, 2005; Demirel *et al.*, 2007].

The finding of TAP-like transporters in the plant vacuole by different proteomic approaches encouraged us to investigate the vacuolar transport activity for larger peptides [Endler *et al.*, 2006]. We chose peptides, which had a similar amino acid sequences as used to characterize the human TAP heterodimer mediating peptide transport [Lankat-Buttgereit and Tampé, 2003]. All three fluorescein-labeled peptides tested were transported across the tonoplast in a strictly ATP-dependent way. As expected for an ABC-type catalyzed transport, GTP but not AMP-PMP could substitute for ATP. Furthermore, peptide transport was inhibited by vanadate, but not by bafilomycin or valinomycin. Vanadate inhibition was more pronounced for shorter peptides, whereas the transport of the 27-aa peptide was inhibited only about 50%. Valinomycin increased the transport activities in the case of larger peptides (Fig. 2). This stimulating effect of valinomycin could be related to the excess of positive charges of the peptide and the fact that the longer peptides used in this study contained an increased number of positive charges. Destroying the trans-vacuolar membrane potential may therefore reduce the energy for the transfer of the peptides and this would be most pronounced for the 27 aa peptide, since it contains six net positive charges.

Our data suggests that the vacuole has at least one ABC-type protein that transports peptides from the cytosol into the vacuole. The transporter



exhibited an apparent affinity of approximate 15  $\mu$ M for 9 aa peptides, which is similar to that of the human ABCB9/TAPL (6.8  $\mu$ M) [Wolters *et al.*, 2005]. This high affinity of the transporter would indicate an efficient transport of the peptides from the cytosol into the vacuole. It is likely that the peptides transported into the vacuole are subsequently degraded to free amino acids by vacuolar endoproteases and exopeptidases. We therefore hypothesize that the proteasome and maybe other, so far unknown cytosolic proteolytic activities produce peptides, which are readily transported into the vacuole in order to be degraded and recycled to sustain plant metabolism. Whether peptides generated by plastidic proteases are exported into the cytoplasm and finally transported into the vacuole is so far unknown. TAP-like plant transporters have been localized in the vacuolar membrane using a GFP fusion protein as well as by proteomic approaches [Yamaguchi *et al.*, 2002, Endler *et al.*, 2006]. Further studies will show whether these TAP-like proteins act as long-chain peptide transporters also in plants. Arabidopsis AtTAP2/AtABCB27/ASL1 and the barley TAP, HvID17, have been shown to be related with other processes. HvID17 is strongly induced by iron deficiency and has been proposed to be implicated in iron homeostasis [Yamaguchi *et al.*, 2002]. AtTAP2/AtABCB27, which was also found to be localized in the vacuolar membrane in a proteome study and by using a GFP tagged construct, has been proposed to be involved in aluminium tolerance, since the corresponding knock-out mutant exhibited reduced root growth when grown on Al<sup>3+</sup> containing medium [Jaquinot *et al.*, 2007, Larsen *et al.*,

2007]. Further studies have to be performed to identify which transporter is responsible for the long-chain peptide transport and which role it plays in nitrogen metabolism of the plant.

### **Acknowledgements**

This research was supported in part by grants from the Swiss National Foundation to E.M.

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## Figure legends

**Fig. 1: Time-dependent uptake of peptides into isolated barley mesophyll vacuoles.** Vacuoles were incubated with 2  $\mu$ M of three different fluorescein( $\phi$ )-labeled peptides; 9-mer: RRYC( $\phi$ )KSTEL (A), 18-mer: RRYQKSTELRRYC( $\phi$ )KSTEL (B) and 27-mer: RRYQKSTEL-RRYQKSTELRRYC( $\phi$ )KSTEL (C) in the absence ( $\triangle$ ) or presence ( $\blacktriangle$ ) of 4 mM MgATP. Peptide transport was quantified by fluorescence detection as described in Materials and Methods. At the time points indicated, incubation

was interrupted by removing vacuoles from the incubation medium via centrifugation through silicon oil. Each time point is the mean of 5 replicates, and error bars represent  $S_D$ .

**Fig. 2: Effect of nucleotides and inhibitors on peptide uptake.**

Comparison of the transport activities of labeled 9-mer (A), 18-mer (B) and 27-mer (C) peptides in response to nucleotides (MgATP, MgGTP and AMP-PNP, 4 mM) and inhibitors (0.5 mM vanadate, 10  $\mu$ M valinomycin and 0.1  $\mu$ M bafilomycin). Peptide transport was quantified by fluorescence detection and transport activities were related to transport in the presence of MgATP (100%). Values are means of two to three independent experiments each with 5 replicates, error bars represent  $S_D$ .

**Fig. 3: Inhibition of 9- and 27-mer peptide uptake as a function of ortho-vanadate concentration.**

Uptake of fluorescein-labeled 9-mer (■) and 27-mer (▲) peptides into barley mesophyll vacuoles was determined in the presence of increasing ortho-vanadate concentrations. Transport was carried out in the presence of 4 mM MgATP.

**Fig 4. MgATP concentration dependent uptake of the 9-mer peptide**

ATP dependency of the fluorescein-labeled 9-mer (■) transport activity was established by increasing MgATP concentrations. Barley mesophyll vacuoles were incubated for 20 min in the presence of 2  $\mu$ M 9-mer peptide. MgATP concentrations were kept constant by the addition of phosphocreatine (10



mM) and phosphocreatine kinase ( $16 \text{ U} \cdot \text{ml}^{-1}$ ). Peptide transport was quantified by fluorescence detection and inhibition of the transport activity was related to transport in the absence of vanadate (100%). Results are means of two experiments per peptide. Each concentration is the mean of two independent experiments, each with 5 replicates and error bars represent  $S_D$ .

**Fig. 5. Concentration-dependent uptake of the 9-mer peptide in barley mesophyll vacuoles.**

Vacuoles were incubate for 20 min in the presence of 4 mM MgATP and fluorescein-labeled peptide (RRYC( $\Phi$ ) KSTEL). Concentration dependence of the peptide transport activity was determined by increasing peptide concentrations. The data were fitted by the Michaelis-Menten equation. Peptide transport was quantified by fluorescence detection. Each concentration is the mean of 5 replicates and error bars represent  $S_D$ .

**.Fig. 6. Inhibition of the uptake of the 9-mer peptide by peptides of increasing size.** Transport activities were determined by incubating barley mesophyll vacuoles in the presence of fluorescein-labeled 9-mer peptide (RRYC( $\Phi$ )KSTEL), 4 mM MgATP and one of the non-labeled randomized peptide libraries of different length ( $X_i$ ,  $i = 4, 7, 10, 11, 17, 23, 35$  and 53 residues, see Materials and Methods). The concentration of labeled peptide was  $2 \mu\text{M}$ , non-labeled peptides were added at a 10 fold excess ( $20 \mu\text{M}$ ) and

incubation time was 20 min. Peptide transport was quantified by fluorescence detection and transport rates were related to transport in the absence of an unlabeled peptide (100%). The data represent means of two to three independent experiments each with 5 replicates for each X<sub>7</sub>-mer peptide, error bars represent S<sub>D</sub>.

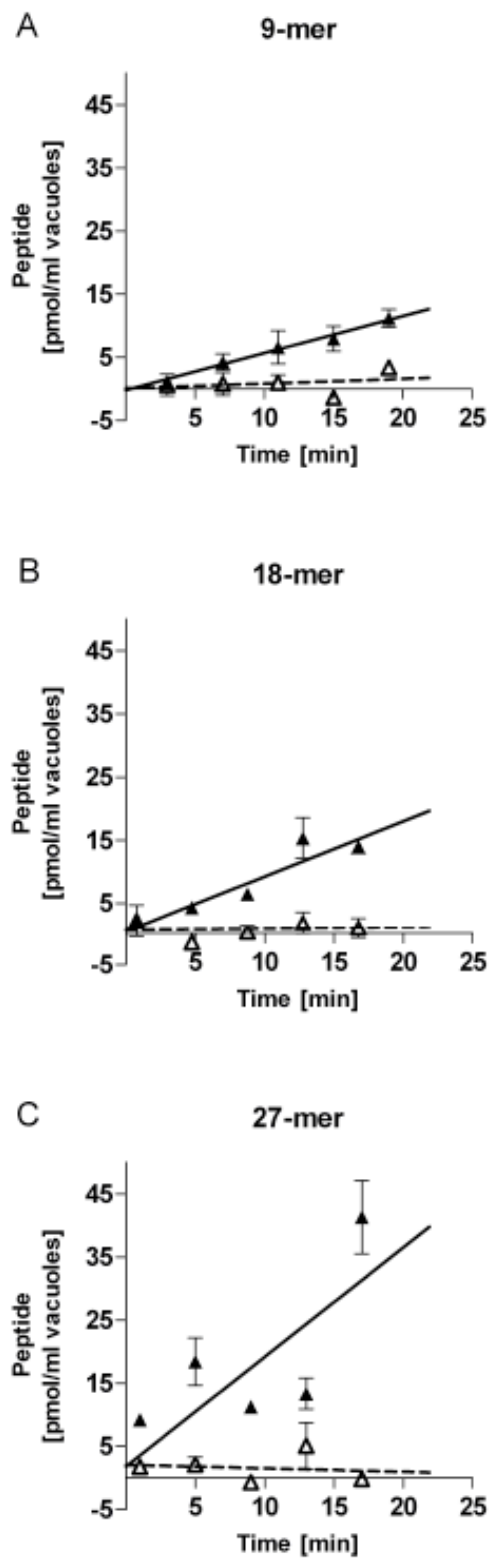


Figure 1

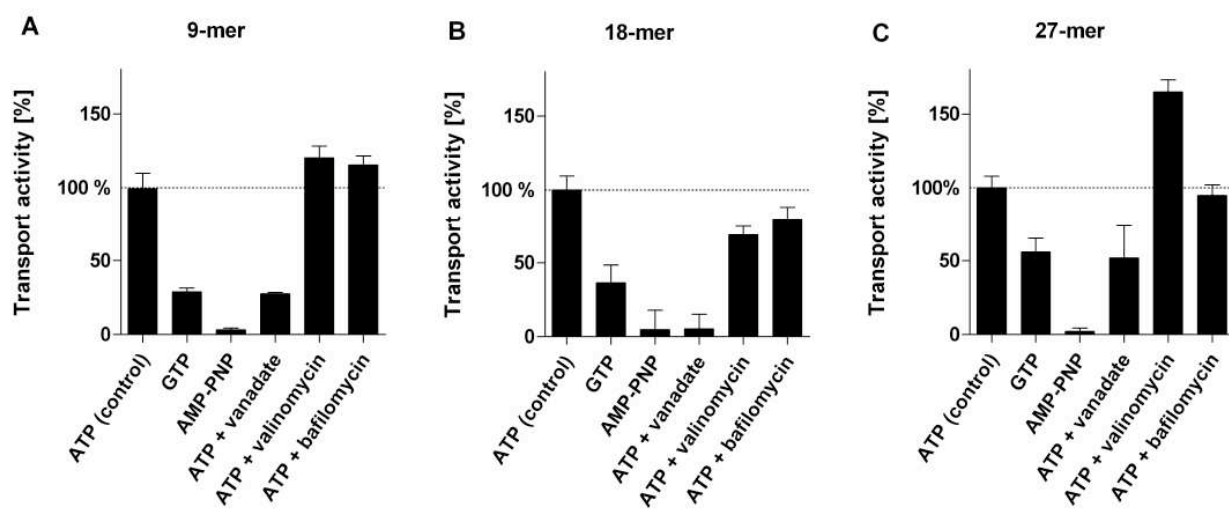


Figure 2

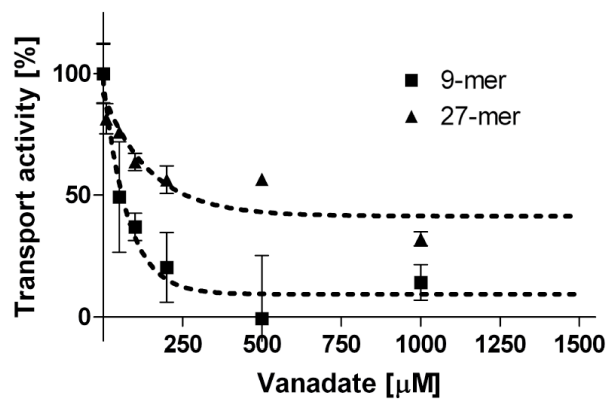


Figure 3

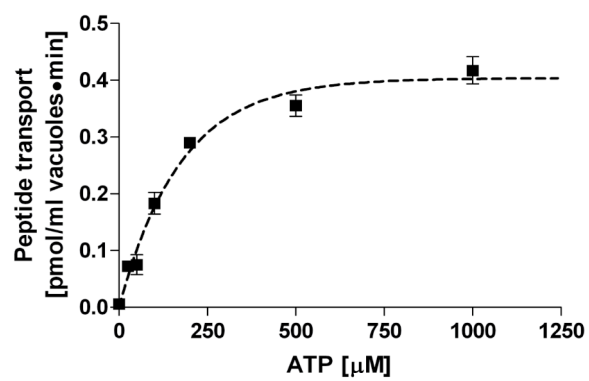


Figure 4

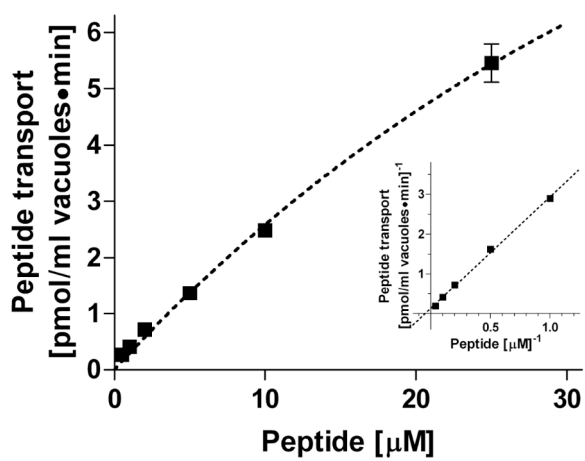


Figure 5

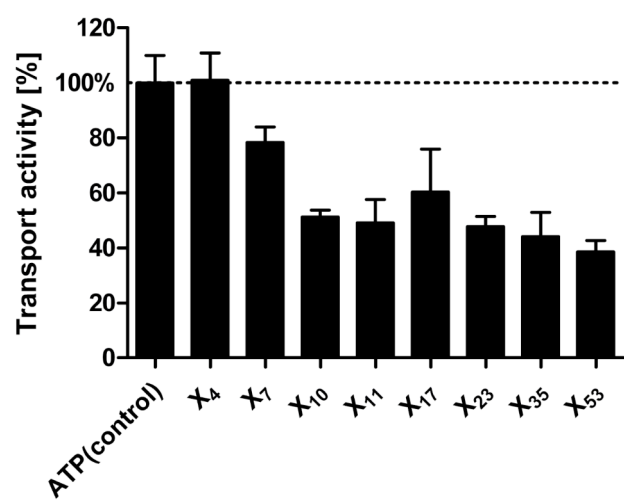


Figure 6